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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 02:31:42 : Search time 180.75 seconds
(without alignments)
2290.944 Million cell updates/sec

Title: us-09-525-998a-1_copy_121_603

Perfect score: 483

Sequence: 1 gatattgtgtgtcccaagg.....gactaccccgattgagat 483

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 930621 seqs, 42962619 residues

Total number of hits satisfying chosen parameters: 1461342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_1101.*

1:	/SIDS2/gcgdata/geneseq/geneseq/NA1980.DAT.*
2:	/SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT.*
3:	/SIDS2/gcgdata/geneseq/geneseq/NA1982.DAT.*
4:	/SIDS2/gcgdata/geneseq/geneseq/NA1983.DAT.*
5:	/SIDS2/gcgdata/geneseq/geneseq/NA1984.DAT.*
6:	/SIDS2/gcgdata/geneseq/geneseq/NA1985.DAT.*
7:	/SIDS2/gcgdata/geneseq/geneseq/NA1986.DAT.*
8:	/SIDS2/gcgdata/geneseq/geneseq/NA1987.DAT.*
9:	/SIDS2/gcgdata/geneseq/geneseq/NA1988.DAT.*
10:	/SIDS2/gcgdata/geneseq/geneseq/NA1989.DAT.*
11:	/SIDS2/gcgdata/geneseq/geneseq/NA1990.DAT.*
12:	/SIDS2/gcgdata/geneseq/geneseq/NA1991.DAT.*
13:	/SIDS2/gcgdata/geneseq/geneseq/NA1992.DAT.*
14:	/SIDS2/gcgdata/geneseq/geneseq/NA1993.DAT.*
15:	/SIDS2/gcgdata/geneseq/geneseq/NA1994.DAT.*
16:	/SIDS2/gcgdata/geneseq/geneseq/NA1995.DAT.*
17:	/SIDS2/gcgdata/geneseq/geneseq/NA1996.DAT.*
18:	/SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT.*
19:	/SIDS2/gcgdata/geneseq/geneseq/NA1998.DAT.*
20:	/SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT.*
21:	/SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT.*
22:	/SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	483	100.0	483	19	AAV41548 Human soluble tumo
2	483	100.0	483	19	AAV19801 Soluble tumour nec
3	483	100.0	483	20	AAV81732 Tumour necrosis in
4	483	100.0	483	22	AAV81945 Human 30 kDa TNF i
5	483	100.0	1301	18	AAV94022 cDNA for TNF(20 19
6	483	100.0	1334	11	AAQ06282 Plasmid tumour nec
7	483	100.0	1368	14	AAQ49932 Lambda-derived TNF
8	483	100.0	1464	21	AAQ45105 Human TNF1 coding
9	483	100.0	1478	20	AAV58150 Cdc-fusion polype
10	483	100.0	2062	13	AAQ29973 TNF-alpha binding
11	483	100.0	2062	13	AAQ24440 Encodes TNF-alpha

12	483	100.0	2088	12	AAQ19883 483: INF inhibitor
13	483	100.0	2088	22	AAQ83446 Human 30 kDa INF i
14	483	100.0	2111	12	AAQ23337 Encodes human 55kD
15	483	100.0	2111	20	AAZ09179 Human tumour necro
16	483	100.0	2161	21	AAZ48475 Human tumour necro
17	483	100.0	2175	16	AAQ90513 p55 INF-R gene, H
18	483	100.0	6889	17	AAV15931 INF-R/intron (WIRAS
19	483	100.0	6926	18	AAV03431 Vector pCDNA3-1g31
20	481.4	99.7	2141	11	AAQ06285 Human Tumour Necro
21	481.4	99.7	2176	12	AAQ22215 Type 1 TNF recepto
22	479.8	99.3	2170	14	AAQ50870 p55 Tumour necrosi
23	478.4	99.0	508	13	AAQ24441 Encodes truncated
24	476	98.3	1117	18	AAV94021 cDNA for TNF(20-19
25	424.4	87.9	1049	19	AAV94037 cDNA for TNF(20-19
26	424.4	87.9	1202	18	AAV94099 cDNA for TNF(20 16
27	415	85.9	1574	21	AAZ50196 Male fusion plasm
28	403	79.3	504	14	AAQ24445 Encodes truncated
29	357.2	71.0	474	13	AAQ24442 Encodes truncated
30	312.2	64.5	339	19	AAV19804 Truncated SINRF, S
31	308	63.8	333	19	AAV19805 Truncated SINRF, S
32	294.2	61.0	332	19	AAV19807 Truncated SINRF, S
33	299.2	61.9	5870	21	AAV15044 Nucleotide sequenc
34	297.4	61.6	2173	11	AAQ06264 Rat Tumour Necrosi
35	294.6	61.0	515	19	AAV19808 Truncated SINRF, S
36	273.8	56.7	294	19	AAV19808 Truncated SINRF, S
37	264.6	54.8	295	19	AAV19807 Truncated SINRF, S
38	258	53.4	1497	21	AAZ50194 Male fusion plasm
39	257.8	53.4	477	13	AAQ24444 Encodes truncated
40	250.8	51.9	1464	21	AAZ50195 Male fusion plasm
41	221.8	45.7	162	13	AAQ23413 Encodes truncated
42	152.8	31.6	1358	21	AAV95103 Partial sequence o
43	132.4	27.4	1027	12	AAQ10878 Gene for TNF-1 for
44	132.4	27.4	1027	22	AAV94043 Partial human TNF
45	58	12.0	2254	21	AAV95104

ALIGNMENTS

RESULT	1
AAV41548	
10	AAV41548 Standard: cDNA: 483 BP.
XX	AAV41548:
AC	AAV41548:
XX	28-SEP-1998 (first entry)
EE	Human soluble tumour necrosis factor receptor type 1:
XX	
XX	Human, tumour necrosis factor, soluble, INF receptor type 1:
KW	Human, tumour necrosis factor, soluble, INF binding protein:
KW	Gene for TNF-1 for
XX	Human sapiens.
US	
XX	
PH	Location/Qualifiers
ET	1:483
ET	/*tag - a
ET	/product- *human soluble TNF receptor type 1*
XX	
XX	WO9824463-A2.
XX	
PD	11-JUN-1998.
XX	
XX	08-DEC-1997: 97W-9522733.
XX	
XX	99-JUN-1997: 97G-052023.
XX	96-DEC-1996: 96S-0032587.
PP	23-JAN-1997: 97S-0036355.
PP	07-FEB-1997: 97S-0039315.
XX	
PA	(AAQ15) AMQIN TNF.
XX	

QY 301 ttcagtgcttcaattgcaacgtctctgctcaatgggaagtgctgacacctctctgtgcaggaag 360
 DB 301 ttcagtgcttcaattgcaacgtctctgctcaatgggaagtgctgacacctctctgtgcaggaag 460
 QY 361 aaacaaagacacgtgtatcacactaccatgcaaggttcttcttctaaagaaagaaagatgtatc 420
 DB 361 aaacaaagacacgtgtatcacactaccatgcaaggttcttcttctaaagaaagaaagatgtatc 420
 QY 421 tcttgaatgaactgaaagaaagccttgaagtgacgaaggttctgcttaccacagattgaag 480
 DB 421 tcttgaatgaactgaaagaaagccttgaagtgacgaaggttctgcttaccacagattgaag 480
 QY 481 aat 483
 DB 481 aat 483
 RESULT 3
 AAV81732 standard; cDNA: 483 BP.
 XX
 AC AAV81732;
 DB 04-MAR-1999 (first entry)
 XX
 DE Tumour necrosis inhibitor 30 kDa encoding cDNA.
 XX
 KW Tumour necrosis factor receptor 1, TNFR-1; inhibitor, osteoprotegerin;
 FW opo; chimeric; fusion; dimerisation domain; autoimmune disease;
 KW inflammation; apoptosis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..483
 FT /tag- a
 FT /note= "no stop codon given"
 XX
 FN W09849305-A1.
 XX
 PD 05-NOV-1998.
 XX
 DE 29-APR-1998; 98W0-US08631.
 XX
 PR 01-MAY-1997; 97US-0850188.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Boyle WJ, Wooden S;
 DR WPI: 1998-034661/03
 DR P-PSDB: AAW89233.
 XX
 DE New chimeric osteoprotegerin polypeptides - contain the
 PI osteoprotegerin dimerisation domain and a heterologous sequence,
 PT useful to treat TNF and TNFR mediated disorders
 XX
 PS Disclosure; Fig 2; 92pp; English.
 XX
 CC The present invention describes a chimeric polypeptide (A1), comprising
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
 CC amino acid sequence. Also described are: (1) a multimer polypeptide
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid
 CC sequence; and (4) a host cell transformed or transfected with the
 CC expression vector so that the nucleic acid is expressible. The products
 CC from the present invention are useful to treat a variety of disorders
 CC including those related to receptor binding. Compositions comprising
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
 CC autoimmune diseases and disorders related to excessive apoptosis. The
 CC chimeras are also useful for detecting molecules which interact with
 CC fused heterologous sequences to identify potential new receptors and

CC ligands. The present sequence encodes the TNF inhibitor 30 kDa protein.
 XX
 SQ Sequence 483 BP; 130 A; 124 C; 123 G; 106 T; 0 other;
 Query Match 100.0%; Score 483; DB 20; Length 483;
 Best local Similarity 100.0%; Pred. No. 4,40-141;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 gataatgataatcccccaaaaataataataataataataataataataataataataataataata 60
 DB 1 gataatgataatcccccaaaaataataataataataataataataataataataataataataata 60
 QY 61 aattgac 120
 DB 61 aattgac 120
 QY 121 tgaaggaatatt 180
 DB 121 tgaaggaatatt 180
 QY 181 agcttgcac 240
 DB 181 agcttgcac 240
 QY 241 cgggaac 300
 DB 241 cgggaac 300
 QY 301 ttcagtgcttcaattgcaacgtctctgctcaatgggaagtgctgacacctctctgtgcaggaag 360
 DB 301 ttcagtgcttcaattgcaacgtctctgctcaatgggaagtgctgacacctctctgtgcaggaag 360
 QY 361 aaacaaagacacgtgtatcacactaccatgcaaggttcttcttctaaagaaagaaagatgtatc 420
 DB 361 aaacaaagacacgtgtatcacactaccatgcaaggttcttcttctaaagaaagaaagatgtatc 420
 QY 421 tcttgaatgaactgaaagaaagccttgaagtgacgaaggttctgcttaccacagattgaag 480
 DB 421 tcttgaatgaactgaaagaaagccttgaagtgacgaaggttctgcttaccacagattgaag 480
 QY 481 aat 483
 DB 481 aat 483
 RESULT 4
 AAC83945
 ID AAC83945 standard; DNA: 483 BP.
 XX
 AC AAC83945;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 IC Human 30 kDa TNF inhibitor coding sequence #1.
 XX
 KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
 KW IL-1; inflammatory disease; degenerative disease; human; ss
 XX
 OS Homo sapiens.
 XX
 FN US6143866-A.
 XX
 PD 07-NOV-2000.
 XX
 PR 19-JAN-1995; 95US-0375242.
 XX
 PR 19-JUL-1990; 90US-0555274.
 XX
 PR 18-JUL-1989; 89US-0381080.
 XX
 PR 11-DEC-1989; 89US-0450329.
 XX
 PR 07-FEB-1990; 90US-0479661.
 XX

PA (AMGE-) AMGEN INC.
 XX Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
 PI Vanderslice RW, Vannice J, Kohno T;
 XX WPI: 2001-006443/01.
 DR P-PSDB; AAB37676.
 XX Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
 PT non-native cysteine residue cross-linked with polyethylene glycol,
 FT useful for treating inflammatory and degenerative diseases mediated by
 TNF -
 XX Example 6; Fig 20; 82pp; English.
 XX The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
 CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
 CC novel TNF inhibitors of the present invention are useful as therapeutic
 CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
 CC for treating inflammatory and degenerative diseases mediated by TNF. The
 CC present sequence is the coding sequence for the 30 kDa TNF inhibitor
 CC The 30 kDa TNF inhibitor can inhibit TNF alpha.
 XX
 SQ Sequence 483 BP; 130 A; 124 C; 123 G; 106 T; 0 other;

Query Match 100.0%; Score 483; DB 22; Length 483;
 Best Local Similarity 100.0%; Pred. No. 3.4e-141;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 gatagtgtgtgtcccaaggaaataatataccacctcaaaaataattcgtttgttacc 60
 DB 1 gatagtgtgtgtcccaaggaaataatataccacctcaaaaataattcgtttgttacc 60
 QY 61 aatgacacaaaggaaactacttcttacaataaactatgacagccaggaagatacaaac 120
 DB 61 aatgacacaaaggaaactacttcttacaataaactatgacagccaggaagatacaaac 120
 QY 121 tacaggaagatgag 180
 DB 121 tacaggaagatgag 180
 QY 181 agctgtcccaatgccgaagaaatgggttcaggttgcagatctcttgcacagtggac 240
 DB 181 agctgtcccaatgccgaagaaatgggttcaggttgcagatctcttgcacagtggac 240
 QY 241 caggaacacagatgag 300
 DB 241 caggaacacagatgag 300
 QY 301 ttcacagtcttcaattgcagagctctgcctcaatgcagagagagagagagagagagag 360
 DB 301 ttcacagtcttcaattgcagagctctgcctcaatgcagagagagagagagagagagag 360
 QY 361 aaacagaaacacagtgatgcacgtgcacgtgcacgttcttcttaagagaaacagatgtgc 420
 DB 361 aaacagaaacacagtgatgcacgtgcacgtgcacgttcttcttaagagaaacagatgtgc 420
 QY 421 tctctatataactataaagaaagctgaaatgcacgaagtttgtcctaccccagattgaag 480
 DB 421 tctctatataactataaagaaagctgaaatgcacgaagtttgtcctaccccagattgaag 480
 QY 481 aat 483
 DB 481 aat 483

RESULT 5
 AAT94022
 ID AAT94022 standard; cDNA; 1301 BP.
 XX
 AC AAT94022;
 XX

DT 19-MAR-1998 (first entry)
 XX
 DE CDNA for TBP(20-190)/hCG-beta fusion protein.
 XX
 KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
 KW beta subunit; hCG-beta; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 279..1289
 FT /tag- a
 XX
 XX W09730161-A1.
 XX
 XX 21-AUG-1997.
 XX
 XX 20-FEB-1997; 97WO-US02315.
 XX
 XX 20 FEB 1996; 96US-0011936.
 XX
 XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 XX
 XX Campbell RK, Chappel SC, Jameson BA;
 XX
 XX WPI: 1997-42503b/39.
 DR P-PSDB; AAW33360.
 XX
 XX Hybrid dimeric protein comprising two co-expressed units - each
 PT based on receptor of ligand and a subunit of a heterodimeric
 PT hormone, especially FSH, for inducing follicular maturation
 XX
 XX Example; Pages 39-40, 60pp, English.
 XX
 XX A novel fusion protein, comprises a dimer forming co-expressed amino
 CC acid sequences, each consisting of a homodimeric or heterodimeric
 CC receptor chain of ligand, with ligand receptor binding activity,
 CC bound directly or via a peptide linker to a subunit of a
 CC heterodimeric protein hormone capable of forming a heterodimer with
 CC the hormone's other subunits. The fusion protein, e.g. the
 CC thrombopoietin (TPO)/human chorionic gonadotrophin beta subunit
 CC (hCG-beta) fusion protein encoded by the present sequence,
 CC significantly increases the biological activity of the hormone
 CC component, reducing the requirement for hormone itself and the
 CC number of injections needed.
 XX
 XX Sequence 1301 BP, 259 A, 413 C, 351 G, 268 T; 0 other;

Query Match 100.0%; Score 483; DB 18; Length 1301;
 Best Local Similarity 100.0%; Pred. No. 5.4e-141;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gatagtgtgtgtcccaaggaaataatataccacctcaaaaataattcgtttgttacc 60
 DB 345 gatagtgtgtgtcccaaggaaataatataccacctcaaaaataattcgtttgttacc 404
 QY 61 aatgacacaaaggaaactacttcttacaataaactatgacagccaggaagatacaaac 120
 DB 405 aatgacacaaaggaaactacttcttacaataaactatgacagccaggaagatacaaac 464
 QY 121 tgcaggaagatgag 180
 DB 465 tgcaggaagatgag 524
 QY 181 agctgtcccaatgccgaagaaatgggttcaggttgcagatctcttgcacagtggac 240
 DB 525 agctgtcccaatgccgaagaaatgggttcaggttgcagatctcttgcacagtggac 584
 QY 241 caggaacacagatgag 300
 DB 585 caggaacacagatgag 644

PD 31-AUG-2000
 XX 23-FEB-2000: 2002WC-US04506.
 XX 23-FEB-1999: 99US 0121314.
 XX (GENA-) GENAISSANCE PHARM INC.
 PA (NAND-) NANDABALAN K.
 PA (SCHU-) SCHULZ V P.
 PA (STEP-) STEPHENS J C.
 PA (CHEW-) CHEW A.
 XX
 PI Nandabalan K, Schulz VP, Stephens JC, Chew A;
 XX WPI: 2000-543909/49.
 XX P-PSDB: AAB23446.
 XX
 PT Polynucleotides comprising polymorphic variants of a reference sequence
 PT for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
 PT biological function of TNFR1 and identifying drugs targeting the
 PT protein for treating disorders -
 XX
 PS Claim 7; Fig 4; 79pp; English.
 XX
 CC The present invention relates to polymorphic variants of the tumour
 CC necrosis factor receptor 1 (TNFR1) gene. The present sequence is
 CC the coding sequence of the TNFR1 gene. The sequence of the whole gene is
 CC given in AAA95102, AAA95103 and AAA95104. The polymorphisms were
 CC identified by amplifying and sequencing regions of the gene. Twelve
 CC polymorphic loci were discovered. Of these twelve polymorphisms, four can
 CC cause a change in the TNFR1 protein. The TNFR1 polymorphisms may be
 CC useful for studying the biological function of TNFR1 as well as for
 CC identifying drugs targeting the protein for treatment of disorders
 CC related to its abnormal expression or function such as tumours,
 CC apoptosis related disorders and bacterial infection.
 XX
 SQ Sequence 1388 BP: 292 A; 424 C; 276 G; 276 T; 0 other;

Query Match: 100.0%; Score 483; DB 21; Length 1368;
 Best local Similarity 100.0%; Pred. No. 5,4e-141;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gataagtgatgaccccaagaaataatatacaaccccaaaatgaatgagtgatgac 60
 DB 121 gataagtgatgaccccaagaaataatatacaaccccaaaatgaatgagtgac 180
 QY 61 aatgacacaaagaaactactgtgacaaatgactgacagggccggaggaatagaa 120
 DB 181 aatgacacaaagaaactactgtgacaaatgactgacagggccggaggaatagaa 240
 QY 121 tcaaggagatgacagagctcttccagcttccagcttccagcttccagcttccagct 180
 DB 241 tcaaggagatgacagagctcttccagcttccagcttccagcttccagcttccagct 300
 QY 191 aatgacacaaagaaactactgtgacaaatgactgacagggccggaggaatagaa 240
 DB 301 aatgacacaaagaaactactgtgacaaatgactgacagggccggaggaatagaa 360
 QY 241 cggacacccatgactgacagagaaacccatgacagagaaacccatgacagagaa 300
 DB 361 cggacacccatgactgacagagaaacccatgacagagaaacccatgacagagaa 420
 QY 301 ttcagtgcttcaatgacagctctgctcaatgacagagagagagagagagagag 360
 DB 421 ttcagtgcttcaatgacagctctgctcaatgacagagagagagagagagagag 480
 QY 361 aaacagac 420
 DB 481 aaacagac 540
 QY 421 ttcagtgcttcaatgacagctctgctcaatgacagagagagagagagagagag 480

Db 541 ttcagtgcttcaatgacagagagagagagagagagagagagagagagagagag 600
 QY 481 aat 483
 III
 Db 601 aat 603
 RESULT 9
 AAX58150
 ID AAX58150 standard: DNA; 1478 BP.
 XX AC AAX58150:
 XX
 DT 21-JUL-1999 (first entry)
 XX
 DF CadC fusion polypeptide coding sequence.
 KW CadC: fusion protein; tumour necrosis factor alpha interaction domain;
 KW protein-protein interaction; periplasmic domain; transmembrane domain;
 KW CadC transcriptional regulatory domain; receptor interaction;
 KW ligand identification; orphan receptor; ss.
 XX
 OS Synthetic.
 XX
 FN W09923116-A1.
 XX
 IN 14-MAY-1999.
 XX
 IN 03-NOV-1998; 98WO-US23407.
 XX
 PP 06-SEP-1998; 98US-0149922.
 PP 03-NOV-1997; 57US-0064058.
 XX
 PA (SMALL-) SMALL MOLECULE THERAPEUTICS INC.
 XX
 PI Hsing W, Menzel R, Taqqart PA;
 XX
 XX WPI: 1999-313305/26.
 XX
 PT New CadC fusion polypeptide nucleic acid constructs
 PS Claim 4; Fig 9a, 123pp; English.
 XX
 CC This sequence encodes a CadC-fusion polypeptide containing the
 CC tumour necrosis factor alpha interaction domain.
 CC The invention relates to CadC fusion polypeptide nucleic acid constructs,
 CC which are used to transform cells to produce systems for identifying
 CC compounds which modulate interactions between protein sequences. The
 CC CadC-fusion polypeptides comprise a periplasmic domain, a transmembrane
 CC domain and a CadC transcriptional regulatory domain. Cells transformed
 CC with nucleic acid encoding the fusion proteins and a cadA reporter
 CC construct can be used for identifying compounds which mediate a specific
 CC protein-protein interaction such as modulation of interactions between
 CC protein sequences involved in receptor interactions, e.g. dimerisation.
 CC Such methods can be used for identifying ligands for orphan receptors.
 CC The system is extremely sensitive in that it is based on low and the
 CC magnitude of signal background is quite robust, such that even minor
 CC modifications in protein-protein interactions are readily detectable.
 XX
 SQ Sequence 1478 BP: 398 A; 351 C; 346 G; 361 T; 2 other;

Query Match: 100.0%; Score 483; DB 21; Length 1478;
 Best local Similarity 100.0%; Pred. No. 5,6e-141;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gataagtgatgaccccaagaaataatatacaaccccaaaatgaatgagtgatgac 60
 DB 941 gataagtgatgaccccaagaaataatatacaaccccaaaatgaatgagtgatgac 1000
 QY 61 aatgacacaaagaaactactgtgacaaatgactgacagggccggaggaatagaa 120
 DB 1001 aatgacacaaagaaactactgtgacaaatgactgacagggccggaggaatagaa 1060

KW autoimmune disease; rheumatoid arthritis.

XX Homo sapiens

XX Key: Location/Qualifiers

XX CDS 156..1517

XX /product= human TNF-alpha

XX /tag= a

XX mat_peptide 1265..1267

XX /tag= b

XX /note= #3

XX mat_peptide 1265..1267

XX /tag= c

XX /codon= seq:"10C", aa:Thr

XX 1258..1260

XX /tag= d

XX /codon= Seq:"AC", aa:Leu

XX 1433..1435

XX /tag= e

XX /codon= Seq:"GAC", aa:Asn

XX 156..174

XX /tag= f

XX W09207076-A.

XX 30-APR-1992.

XX 18-OCT-1991; 91W0-GB01826.

XX 18-OCT-1990; 90GH-0022648.

XX (CHAR-) CHARING CROSS SUNLEY RES CENT.

XX Brennan FM, Feldmann M, Gray PW, Turner MJC.

XX W01; 1992-167156/20.

XX P-PSDB; AAN24000.

XX New polypeptide capable of binding human TNF alpha - comprises
PT first three cysteine-rich subdomains of TNF alpha receptor for
PT treating autoimmune disease, septic shock, HIV etc.
XX Claim 4; Fig 1; 43pp; English.

CC This sequence encodes human TNF alpha 55kD receptor . A placenta cDNA
CC library in cDNA was screened with probe AAQ2923. Ten hybridising clones
CC were plaque purified and cDNA size determined by PAGE against an
CC Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC sequenced. The coding region of the majority of the human TNF-alpha
CC 55kD receptor was isolated as an EcoRI fragment encoding 374 amino
CC acids, and cloned into a mammalian cell expression vector, resulting
CC in pTNFR. A derivative of the TNF-alpha receptor was produced by
CC engineering a termination codon just prior to the transmembrane
CC domain. PCR with primers AAQ2923.8 generated a submp
CC restriction fragment which was cloned into pTNFR, giving pTNFRcd.
CC DNA sequencing confirmed this contained the designed DNA sequence.
CC The TNF-alpha receptor expression plasmids were then transfected
CC into monkey COS-7 cells.
CC See also AAQ24440-51, AAN24000, AAN24000-84, AAN24585, AAQ29236-8
XX Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T; 0 other;

Query Match 100.0%; Score 483; DB 13; Length 2062;
Best Local Similarity 100.0%; Pred. No. 6.5e-141;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 gatagtatgtctcccaagaaataatatacccccctcaaaaataattccatttgcgtacc 60
Dh 275 gatagtatgtctcccaagaaataatatacccccctcaaaaataattccatttgcgtacc 334
OY 61 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 120

Dh 335 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 394
OY 121 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 180
Dh 335 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 454
OY 181 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 240
Dh 455 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 514
OY 241 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 300
Dh 515 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 574
OY 301 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 360
Dh 575 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 634
OY 361 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 420
Dh 635 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 694
OY 421 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 480
Dh 695 agtgcgcacaaagaaatctatgtacaaatgacttccaggccggccagatcagac 754
OY 481 aat 483
Dh 755 aat 757

RESULT 12

AAQ10883

ID AAQ10883 standard; cDNA; 2068 BP.

XX AAQ10883;

XX 13-MAY-1991 (first entry)

XX 30kD TNF inhibitor precursor gene in lambda-qt10-7ctn1bp.

XX Tumour necrosis factor; inhibitor; ss.

XX Homo sapiens.

XX Key: Location/Qualifiers

XX CDS 171..1536

XX /tag= a

XX AU058976-A.

XX 24-JAN-1991.

XX 16-JUL-1990; 90AJ-0058976.

XX 07-FEB-1990; 90BS-0479661.

XX 18-JUL-1989; 89BS-0381080.

XX 11-DEC-1989; 89BS-0450329.

XX (SYNFE-) SYNFERGEN INC.

XX W01; 1991-073847/11.

XX P-PSDB; AAN10986.

XX Tumour necrosis factor inhibitor - for suppression of TNF alpha
XX and -beta, useful as therapeutic agent.
XX Disclosure; Fig 21; 142pp; English.
XX The sequence encodes the entire 30 kD TNF inhibitor. The clone from
XX which the sequence was obtained was isolated from a cDNA library
XX pred. from RMA form 2917 cells treated with LPS/PHA. The whole
XX gene can be inserted into expression vectors for prep. of TNF

cc necrosis factor (TNF). The products of the invention have
cc anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
cc to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
cc glomerulonephritis, cerebral malaria, immune responses and inflammation),
cc (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
cc diagnostic determination of TNF in body fluids. Antibodies raised against
cc (I) are used for affinity purification of (I). This sequence encodes
cc a tumour necrosis factor binding protein described in the method of
cc the invention.
xx
SQ Sequence 2111; HP, 445 A, 629 C, 587 G, 450 T, 0 other;

Query Match 100.0%; Score 483; DB 20; Length 2111;
Best local Similarity 100.0%; Pred. No. 6,60-141;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 qataatgataatcccaaaataatataatccaccccaaaaataatcgaatttgcgtacc 60
Db 307 qataatgataatcccaaaataatataatccaccccaaaaataatcgaatttgcgtacc 366
QY 61 aagtaaccacaadgaactacttgtaaatgaactatccaggcccgaggaatcaggac 120
Db 367 aagtgccacaaagaacaaactacttgtaaatgaactatccaggcccgaggaatcaggac 426
QY 121 tcaagggaatgataagcggcctcttccacgcttcagaataaccaccccaagacacgcctc 180
Db 427 tgcagggaatgataagcggcctcttccacgcttcagaataaccaccccaagacacgcctc 486
QY 181 agctgctcccaatgcccaaaagaataatcgaatcgaatggaatctctttacacaaatgac 240
Db 487 agctgctcccaatgcccaaaagaataatcgaatcgaatggaatctctttacacaaatgac 546
QY 241 cgggaacacgtgtgtggtgcaggaagaacccagtaaccgcaattattggaagtgaataacctt 300
Db 547 cgggaacacgtgtgtggtgcaggaagaacccagtaaccgcaattattggaagtgaataacctt 606
QY 301 ttcgaatgcttcaatcagaacctctacclcaalgggaacccgtacacccctccctgcccagag 360
Db 607 ttcgaatgcttcaatcagaacctctacclcaalgggaacccgtacacccctccctgcccagag 666
QY 361 aacacaaacccgtatgacccctgacatgacgatttcttctaaagaaacaaacgaatgatac 420
Db 667 aacacaaacccgtatgacccctgacatgacgatttcttctaaagaaacaaacgaatgatac 726
QY 421 tccgtgtatgaactatataaaagacccctggagtgacagaaattgtgcctacccagattgag 480
Db 727 tccgtgtatgaactatataaaagacccctggagtgacagaaattgtgcctacccagattgag 786
QY 481 aat 483
Db 787 aat 789

Search completed: April 24, 2002, 9:28:29
Job time: 3407 sec